

338/550

FIGURE 338

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSS
QPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGFPYSC
SVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSKFAVQYQWDR
QLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLLEVSTGPAAVVAG
AVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDIAIAPRTLFWPKSSDTISKNGTLSSVTS
ARALRPPhGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPISPIPGGVSSSGLSRMGAVPV
MVPAQSQAAGSLV

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

339/550

FIGURE 339

GCGAGAACCTTTGCACGCGCACAAACTACGGGGACGATTTCTGATTGATTTTGGCGCTTTCGATCCACCCCTCT
 CCGTTCTC**ATGG**GAGCTTTGGGGACAAAGCGTCCCGACCGCTCGAGCGCTCGAGCAGGGCGGTATCCAGGAGGCA
 GGAAGCGCTGGAGAACCGACGACCGATCTGCTTGGAGCCCAAGATCTTAAGTTGCTGTCTTCATCTCAGTCAGTAACTGTA
 TGCTGCGCGGTCCGGGTGACTCTGCCACCATCCCCGGCGAGGACGAGTCCCCCAGACAGACAGTGGGCCACACAG
 AACAGAGGGCGCAGCTCAAGGAGGAGGAGTCCAGCAGGATCTCATAGTCAGAAATATATCTGGAGCGCTGTAAAC
 CGTGCACAGAGGGTGTGGATTACACCATTGCTTCCCAACATTTGGCTTCTTGGCTGCTATGTACAGTTTGTAAAT
 CAGGTCAACACAAATAAAGTTTCTGTACACGACACAGAGACACCGTGTGTGTCAGTGTGAAAAAGGAGGCTTCAGAG
 ATAAAACTCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCAGAGGGATGCTCAAGGTCAGTAACTGTA
 CGCCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTCCCATCGGAAAACCCAGCAGCGGAGGAGA
 CAGTGACCAACCATCTCTGGGGATGCTTGCCCTTCCCTATCACTACCTTATCATCATAGTGGTTTTAGTCATCATTT
 TAGCTGTGGTTGTGGTTGGCTTTTCATGTCCGAGAAATTCATTTCTTACCTCAAAGGCATCTGCTCAGGTGGTG
 GAGGAGGTCCGAACTGTGCACAGAGTCTTTTCGGGGCGGTTTCATGTCTTACAGAGTTCCTGGGGCGGAGG
 ACAATGCCCGAACAGACCTCAGTAAACAGATACTTGCAGCCACCCAGGTCTCTGAGCAGGAAATCCAGGTC
 AGAGAGTCCGACAGCTAACAGGTGTGACTGTAGAGTCGCCAGAGGAGCCACAGGCTCTGCTGGAACAGGCAGAAG
 CTGAAGGGTGTGAGAGGAGGAGGCTCTGGTTCCAGTGAATGACCGTGACTCCGCTGACATCAGCACCTTGTGGT
 ATGCTCTCGGCAACACTGGAAGAAGGACATGCAAGGAAACAACTCAGGACCAACTGGTGGGCTCCGAAAGGCTCT
 TTTATGAAGAAGATGAGGACAGGCTCTGCTACGCTCGCTTGAAGAAGATCTCTCAGGAAACAGAGCTTCCCT
 CATTTACCTTTTCTCTCAAAAGGGGAGCAGCGCTGGAAGAAGACAGTCAGTACTTGAACCATGCCCCAACAACT
 CTACTATCCAAATATGGGCGAGCTTACCAATGGTCTCAGAACTTGTTAACCGCATGGAGTAATTTATTGAAGAT
 ACTCGGTGTGATGAAGCAACGGGAGAAATTTATATCAGATTCTTGGCTGCTAGTTATACGATTTGTATTAAGG
 TCTGCTTTAGGGCCATGCGGTGGCTCATGCTGTAACTCCAGCACTTTGATAGGCTGAGGCGAGGTGGATTGCTT
 GAGCTCGGGAGTTTGAAGACAGGCTCATCAACACAGTGAACCTCCATCTCAATTAAGGAGAAAAAGTGGTTT
 TAGGATGTCACTTTTTCAGTTCTCATCATGAGACAGTCTTTTCTGCTTCTTATATGCAAGCTCCATCT
 CTACTGCTGTGTCATTTAATGACATCTAACTACAGATGCCCGACAGCCAAATGCTTTGCCCTTATAGTTTATTA
 ACTTTAGAACCGGATATCTGTTTAACTCTATTTTTCAGTTTCGGATATTTGACTTAATGATGAGATTATC
 AAGACGTAGCCCTATGTCTAAGTCTAGCATATGGACTTACGAGGTTCCAGCTTAGAGTTTGAAGCTTTAAGATA
 GGATTAATGGGGCTTACCCCCACCTTAATTAGAGAAACATTTATATGCTTACTACTGTAGGCTGTACATCTCTT
 TCCGATTTTGTATAATGATGTAACATGGAAAACTTTAGGAATGCACCTATTAGGCTGTTTACATGGGTTG
 CCTGGATACAAATCAGCAGTCAAAAAAGTAAATAATTAAGTGTGACGGAGGAGAAATCCTCCCTCTGTGGG
 AGGCACCTACTGCATTCCAGTTCTCCCTCTCGGCCCTGAGACTGGACACAGGGTTTGTGGCTGGCAGCTTCTCA
 AGGGGCGAGCTTGTCTTACTTGTAAATTTAGAGGTATATAGCCATATTTATTTATAAATAAATATTTATTAATTT
 ATTTATAAGTAGATTTTACATATGCCCAGGATTTGAAGAGCCTGGTATCTTTGGGAAGCCATGTGCTGGTTT
 GTCTGCTGTGGGACATCTGGGACTGCATCTTCCGACTTGTCCACAGAGATGAGGACAGTGAAGATTAAGTTAG
 ATCCGAGACTCGCAGAGCTTCTCTTCAAGCGCCATTACAGTTGACGTTAGTGAATCTTACGCTCATTTGGG
 CTCAGGCGAGAGCAGGTGTTATCTGCCCGGCACTTCCCATGGCATCAAGAGGGAAGAGTGGACGGTGTGGG
 AATGGTGTGAATATGGTGGCACTCAGGCATGGATGGGCGGCTCTCGCTTCTGGTGGTCTGTGAAGTGAAGTCTCT
 GGGATGCTTTTAGGCGAGAGATCTCTGAGCTGGTTTAGGTACAGATCCCTGTTTAGGAGGCTTGGCGCCT
 CTGTAAGCATCTGCATCATCTCAGAGATATCAATTTCTTAAACACTGTGACAAACGGGATCAAAATGGCTGACACA
 TTTGCTCTCTGTCACGTTCCATTTATTTATTTAAACCTCAGTAATCTTTAGTCTCTTTCCAGCAAACTCT
 TCTCCACAGTAGCCAGTCTGTGGATAGATAAATACGGATATAGTCATTCTAGGGGTTTCAGTCTTTTCCATCTC
 AAGCACTTGTGTGTTTGTGCCGGACTGGTTGGCTGGGACAAAGTTAGAACTTCCCTGAAGTTCGCACATTCAG
 ATGTTGTGTCCATGGAGTTTTAGGAGGGGATGGCTTTCGGCTCTTCGCACTTCCATCTCTCCACTTCCATC
 TGGGCTCCCAACCTTGTCCCTGCTCTGCGATGACACAGGGTGTGCTGCTCTCTAGTCTTGTGCTTGTGCTGCTG
 GGGCTTCTGTGAGGAGACTTGTCTCAAAGCTCAGAGAGAGCCAGTCCGGTCCGAGTCTTGTGCTTGTGCTCTC
 AGAGGCTCTCTTGTGAAGATGCATCTAGACTACCGCTTATCAGTTTAAGCTTCTTCTTAACATGAAGCTTC
 CTGACAACATGAATTTGTGGGGTTTTTGGCGTGTGTTGATTTGTTTAGGTTTTGCTTTATACCGGCGCAAAAT
 AGCACATAACACCTGGTTATATATAAATACTCATATGTTTATGACCAAAATAAATAGAACTCATRTTAAAT
 AAAAAAATAAATAAATAAATAAATAA

340/550

FIGURE 340

MGLWGQSVPTASSARAGRYPGARTASGTRFWLLDPKILKEVVEIVAVLLPVRVDSATIPRQDEVFQQTVAFAQQQR
RSLKEEECPAGSHRSEYTGACNPGTEGVDYTTASNNLPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSFQDKN
SPEMCRCTCRGCGFRGMVKVSNCTPRSDIKCKNESAAASSTGKTPAAEETVTTILGMLASPHYLIIVVLVILAV
VVVGFSCRKKFISYLGICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQQGQEL
AELTGVTVESPEEPQRLLEQAEAGCQRRRLVVPNDADSADISTLLDASATLEEGLHAKETIQDQLVGSEKLFYE
EDEAGSATSCSL

Important features:**Transmembrane domains:**

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276, 297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

341/550

FIGURE 341

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAGG
CCATGCTTCGTTTCTTGCCAGATTGGCTTTCAGCTTCTGTTAATTCTGGCTTTGGGCCAGG
CAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCACCCC
AGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTTCAGGATCGCGAGGCAGCAGCGA
CCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGAATGTACTTC
GCTTTCTCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCAAGCTTCTCTCTGCC
TGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACATTGGCCC
AGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGAAGCTGGCTC
TGTTCTCTGGTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTAAAAATGTTTG
TGTTGCGGTCACTCCCATGGCCACAAGGTGCTGTTCACCTCAACCTGCTGGATGTAGCTAAGG
ATTGGAATGACAACCCCCGGAATAATTTGCGGTTATTCTCGGAGATACTGGTCAAGAAGATA
GAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGATGCTCCCTTCATG
CTTCCCTGCTGGTGGTGA CTCTCAACCCTGATCAGTGCCACCCTTCTCGGAAAAGGAGAGCAG
CCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCCTGTGCCACCCTCACCAGCTATTCATTAACT
TCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCCCAAGGGGTTTCATGGCAAATTACTGCC
ATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAATTATGCTTTCATGCAAG
CCCTGATGCATGCCGTTGACCCAGAGATCCCCAGGCTGTGTGTATCCCCACCAAGCTGTCTC
CCATTTCCATGCTCTACCAGGACAATAATGACAATGTCAATTCTACGACATTATGAAGACATGG
TAGTCCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAATAGAAGGAGTGTTCTTAGGG
TAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTAGATCGAAATGTC

342/550

FIGURE 342

MLRFLPDLAFSFLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQPVPIILKKIFQDREAAAT
TGVSRDLQVYKELGVRGNVLRFLPDQGGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQ
LGLDLGPNSYYNLGPELELALFLVQEPHVWGQTTTPKPGKMFVLRSVWPQGAHVFNLLDVAKD
WNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTNLNPDQCHPSRKRRAA
IPVPKLSCKNLCHRHQLFINFRDLGWHKWIAPKGFMANYPCHGECPFSLTISLNSSNYAFMQA
LMHAVDPEIPQAVCIPTKLSPISMLYQDNNNDNVILRHYEDMVVDECGCG

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

343/503

FIGURE 343

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCATTCTCTTTTCATTGACAACTGACTTTTTTATTTCT
 TTTTTCATCTCTCTGGGCGAGCTTGGGATCCTAGGCCGCCCTGGGGAAGACATTTGTGTTTTACACACATAAAGGAT
 CTGTGTTTGGGGTTCTCTCTCTCCCTGCACATTGGCATTGCTTAGTGGTTGTGTGGGGAGGAGACCCAGCTGG
 GCTCAGTGTCTGCTTGCACCTTATCTGCCTAGGTACATCGAAGTCTTTTGCAGCTCCATACAGTGATTTGTGCTGTC
 ATCCGCTGGGTATCCTGGGGGCTTGTCTCTGCTGATAGTTGTCTGCTCTGTCTTTACTTCAAAATACACAAC
 GCGCTAAAGCTGCAAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCAACAACCCAGACAGGTGTGTGGGCCAAG
 AACAGCCAGGCGCAAAACCATTTGCCACGGAGTCTTGTCTGCCCTGCAGTGTGTGAAGGATATAGAATTGTGTCC
 AGTTTTGATTCCCTGCCACCTTGTCTGTGCGACATRAATGAGGGCTCTGAGTTAGGAAGGCTCCCTTCTCAAA
 GCAGAGGCTTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGACGGCAGAGAAGAGGCACAG
 CTCCTCATCAGTTTCATGGAAATTAACCTAGTGCTGCTGGGAACCAAGCTGTGGAGATCCCTACAGAGAGCTTC
 CACTGGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGGAATGTGTATAAACAGTCA
 CACAGCTGCTCTATTCTCACACAATCTACCCCTTGCCTGGCTTGGAACTGACGTTTTCCCTGGAGGTGTCCAGAAA
 GCTGATGTAAACAGAGGCTATAAAGCTGTGCGTCTTAAAGCTGCGCCAGCGCTTGGCCAAATGGAGCTGTGA
 AGAAGGCTCATGCCATTGACCTCTTAATTCTCTCTGTTTGGCGGAGCTGACAAATGGCGGAGGCTGAAGGCAAT
 GCAAGCTGCACAGTCAGTCTAGGGGGTGCAATATGGCAGAGACCCAAAGCCATGATCCCTGCACTCAATCCC
 AGTGAGAACTGCACCTGGACAAATGAGAAGACCAGAAAACAAAGCATCAGAAATATCTTTTCCATGTCCAGCTT
 GATCCAGATGGAGCTGTGAAAGTGAAACATTAAAGCTTTTACGGGAACCTCCAGCAATGGGCTCTGCTAGGG
 CAAGTCTGCAGATAAAAGGACTATGTTCTGTATTTGAATCATCATCCAGTACATGAGCTTTCAAATAGTTACT
 GACTCAGCAAGAAITCAAAGAAGCTGCTTTGTCTCTACTACTTCTCTCTCTTAACATCTCTATTCCAACTGT
 GGGCGTTACCTGGATACCTTGGAGGATCCTTCCACAGCCCCAATTACCCAAAGCCGCACTCTGAGCTGGCTTAT
 TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCTAGAAAATAGAC
 AAACAGTGCAAATTTGATTTTTCTTGCCATCTATGATGGCCCTCCACCAACTCTGGCCGTGATTGGACAAGTCTGT
 GGCCGTGTGACTCCCACTTCCGAATCGTCATCAAACCTCTCTGACTGTCTGTGTTGTCTACAGATTATGCCAATTCT
 TACCGGGGATTTTCTGCTTCTTCAACCTCAATTTATGAGAAAACATCAACACTACATCTTTAACTTGTCTCTCT
 TACAGATTGAGATGATTATAAGCAAACTCTACCTAGAGGCTTTAACTCTAATGGGAATAACTCTCAACTAAAA
 GACCCAACTTGCAGACCAAATATCAAAATGTTGTGGAAATTTCTGTCCCTCTAATGGATGTGGTACAATCAGA
 AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCACTCTCAACTCTGAAGTGATCACC
 CGTCAGAAAACACTCCAGATTATTGTGAAGTGTGAATGGGACATAAATCTACAGTGGAGATAATATACATACAA
 GAAGATGATGTAATACAAAGTCAAAATGCATGGGCAATATAACACCAGCATGGGCTCTTTTGAATCCAATTTCA
 TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTGAAACCAAACTCTTTTGTCAAGTTAGTCTGCAC
 ACCTCAGATCCAAATTTGGTGGTGTCTTGATACCTGTAGAGCCTCTCCCACTCTGACTTTGCATCTCCAACC
 TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAACCTGTAAGGTGTATCCCTTATTGGACATCTGGGAGA
 TCCAGCTTTAATGCCCTTAAATCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTTGATATGTGAT
 AGCAGTGACCACAGCTCTCGCTGCAATCAAGSTTGTGTCTCCAGAAGCAACAGAGACATTTCTCATATAAATGG
 AAAACAGATTCCCATCATAGGACCAATCTGCTGAAAAGGGATCGAAGTGAAGTGGCAATTCAGGATTCAGCAT
 GAAACACATTCGGGAAGAACTCCAAACAGCCTTTCAACAGTGTGCATCTGTTTCTTCTTCAAGTGTCTAGCTCTG
 AATGTGGTGACTGTAGCGACAATCACAGTAGGCGATTTTGTAAATCAACGGGAGAGCTACAAATACAGAGCTG
 CAGAACTATTAATACAGAGTCCAAACCTTAAGTGAGACATGTTTCTCCAGGATGCCAAGGAAATGCTACCTCGT
 GGCTACACATTTATGAATAAGTGAAGAGGGCTGAAAGTGACACAGCAGCTGATGTAAAAA

344/550

FIGURE 344

MELVRRIMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTIE
RPNKSIIRIIFSYVQLDPPDGSCSENIKVFDTSSNGPLLGGQVCSKN DYVPVFESSSSTLT FQ
IVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSTSPNYPKPHPELAYCVWHIQVEKD
YKIKLNFKEIFLEIDKQCKFDFLA IYDGPSTNSGLIGQVCGRVTPTFESSNSLT VVLSTDYA
NSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRPKLSNV
VEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITROKQLQIIVKCEMGNSTVEIYYI
TEDDVIQSQNALGKYNTSMALFESNSFEKTI LESPYYVDL NQTLFVQVSLHTSDPNLVVFLDT
CRASPTSDFASTPYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYLQCKVLI CD
SSDHQSRCNQGCVSRSKRDISSYKWKTD SIIIGPIRLKRD RSASGNSGFQHETHAEETPNQPFN
SVHLFSFMVLALNVVTATITVRHFVNQRADYKYQKLQNY

Important features:**Signal sequence:**

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423**Casein kinase II phosphorylation site.**amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 345

[illegible]

346/550

FIGURE 346

MGSRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLGNRNCCRGAGPPPCACRTFFFRVC
 LKHYQASVSPEPPCTYGSVTPVLGVDSFSLPDGGGADSAFNSPIRFFFGFTWPGTFSLII EA
 LHTSDPDDLATENPERLISRLATQRLHTVGEWSSQDLHSSGRTDLKYSYRFVCD EHYH YEGCS
 VFRCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFC DKPGECKCRVGVQGR
 YCDECIRYPGCLHGTCQQPWCNCQEGWGGFLFCNQDLNYCTHHKPCKN GATCTNTGQGSYTC S
 CRPGYT GATCELGIDECDPSPCKNGGSGCTDLENSYSCTCPPGFGY GKICELSAMTCADGPCFNG
 GRCSDSPDGGYSCRCFVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD
 DNVDDCASSPCANGGTCRDGVNDFSCTCPGTYTGRNCSAPVSRCEHAPCHNGATCHERGHRYV
 CECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGQGGPFPWVAVCAGVILVLM LLLGCAAVVV
 CVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKKADFHGDHSADKN
 GFKARYPAVDYNLVQDLKGDDTA VRDAHSKRDTKCQPGQSSGEEKGTP TTLRGGEASERKRPD
 SGCTSKDTKYQSVYVISEEKDECVIATEV

Important features:**Signal sequence:**

Amino acids 1-21

Transmembrane domain:

Amino acids 546-566

N-glycosylation site:

Amino acids 477-481

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 660-664

Tyrosine kinase phosphorylation sites:

Amino acids 176-185; 252-261

N-myristoylation sites:

Amino acids 2-8; 37-43; 40-46; 98-104; 99-105; 262-268; 281-287;
 282-288; 301-307; 310-316; 328-334; 340-344; 378-384; 387-393; 512-518;
 676-682; 683-689; 695-701

Aspartic acid and asparagine hydroxylation sites:

Amino acids 343-355; 420-432; 458-470

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 552-563

EGF-like domain cysteine pattern signature:

Amino acids 243-255; 274-286; 314-326; 352-364; 391-403; 429-441;
 467-479; 505-517

347/550

FIGURE 347

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAACA
TCGTAGTCCACCCCTCCCATCCCCAGCCCCGGGGATTAGGCTCGCCAGCGCCAGCCAG
GGAGCCGGCCGGGAAGCGCG**ATG**GGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGCTGT
TCGCCTGCTGCTGGGCGCCCGGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGGACAT
CTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCTCAAGTGCCAAGTGAAAGATCACGAGG
ACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGAGAGCCC
TTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCAGAGCTCAGCATCAGCATCAGCA
ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGTGCGAACTG
CCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCACTAGTGGTTATAAATCTT
CATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAGCCTGCAGCCC
GGCTCACCTGGAGAAAGGTGACCAAGAAGTCCACGGAGAACCAACCCGCATACAGGAAGATC
CCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCCGGGAGGATGATG
GGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGAGCTGACAGATCCACCTCTC
AACGCATTGAAGTTTATACACCAACTGCGATGATTAGGCCAGACCCCTCCCATCTCTGCTG
AGGGCCAGAAGCTGTTGTACACTGTGAGGGTCGCGGCAATCCAGTCCCCAGCAGTACCTAT
GGGAGAAGGAGGGCAGTGTGCCACCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCTT
TCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGGCAGCTACA
AGGCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCTCCTCTCCAGCACCTACC
ACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTGCTCATCATGCTCATCTTCC
TTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACG
ATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACGACA
AGAAGGAATATTTTCATC**TAG**AGGCGCCTGCCACTTCTGCGCCCCCCAGGGGCCCTGTGGGG
ACTGCTGGGGCCGTCACCAACCCGGACTTGTTACAGAGCAACCGCAGGGCCGCCCTCCCGCTT
GCTCCCCAGCCACCCACCCCTGTACAGAATGTCTGCTTTGGGTGCGGTTTTGTACTCGGT
TTGGAATGGGGAGGAGAGGGCGGGGGAGGGGAGGGTTGCCCTCAGCCCTTCCGCTGGCTT
CTCTGCATTGGGTTATTATTATTTTGTAACAATCCCAATCAAATCTGTCTCCAGGCTGGA
GAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACAACAAAAACA

348/550

FIGURE 348

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWS
NPAQQTLTYFGEKRALRDNRIQLVTSTPHELSSISISNVALADEGEYTCSTFTMPVRTAKSLVTV
LGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFT
VSSSVTFQVTRREDDGASIVCSVNHESLKGADRSTSQRIEVLVYPTAMIRPDPPHPREGQKLLL
HCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLN
VNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLRHKGYLTAEKGSDDAPDADT
AIINAEGGQSGGDDKKEYFI

Important features:**Signal sequence:**

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

349/550

FIGURE 349

ACTTGCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTGCACATGGAGGACAGCAGCAAAG
AGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTACCATACGCCCTCAGGACGTTCCCTCTA
GCTGGAGTTCTGGACTTCAACAGAAACCCATCCAGTCATTTTGATTTTGCCTGTTATTTTTTTTCTTTTCTT
TTTCCCACACATTTGATTTTATTTCCGTACTTCAGAAATGGGGCTACAGACCACAAAGTGGCCAGCCATGGGG
CTTTTTTCCTGAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCAGAGGTGCCAACTCCTGGGCTGCCCTA
GTGTGTGCCGTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTGCCTCTTGGGATCCCGG
AGGGCGTAACCGTACTCTACTCCACAACAACCAAATTAATAATGCTGGATTTCTCTGAGAACTGCACAATGTAC
AGTCGGTGACACGGTCTACCTGTATGGCAACCAACTGGACGAATTCCTCATGAACCTTCCCAAGAAATGTCAGAG
TTCCTCATTGTCAGGAAAACAATATTGAGACCAATTCACGGGCTGCTCTTGGCCAGCTCTTGAAGCTTGAAGAGC
TGCACCTGGATGACAACTCCATATCCACAGTGGGGTGGAAAGACGGGGCCTCCGGGAGGCTATTAGCCTCAAAAT
TGTGTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGACTTGCAAGAGCTGAGAGTGG
ATGAAATCGAATTGCTCTCATATCCGACATGGCTTCCAGAATCTCAGAGCTTGGAGCGTCTTATTGTGGACG
GGAACTCTGACCAACAGGGTATCGCGAGGGCACCCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTG
TACGTAATTGCTGTCCCACCTCTCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGTCAGGACAACC
AGATAAACCACATTCCTTTGACAGCCTTCTCAAACTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAAC
TGGCGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGGAAGCAGCTCACTGCTCGGAATAACCCCTGGT
TTTGTGACTGCAGTATTAATGGGTGACGAATGGCTCAAAATATATCCCTTCATCTCTCAAGCTGCGGGTTTCA
TGTGCCAAGTCTCTGAACAAGTCCGGGGGATGGCCGTGAGGAATTAATATGAATCTTTTGTCTGTCCCAACA
CGACCCCGGCTGCTCTCTTACCCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCCCTCTCTA
TTCAAAACCTAGCAGAACTACACGCTCTCACTCTACACATCGAACTTCCACAGATTCTGACTGGGATG
GCAGAGAAAGAGTGACCCCACTTATTTCTGAACGGATCCAGCTCTCTATCCATTTTGTGAATGATACTTCCATT
AAGTCAGCTGGCTCTCTCTTCCCGTGATGGCATAACAACCTCACATGGGTGAAATGGGCCACAGTTTAGTAG
GGGCACTGTTTCAGGAGCGCATAGTCAGCGGTGAGAAGCAACCTGAGCCTGGTTAACTTAGAGCCCCGATCCA
CCTATCGGATTTGTTTAAAGGAGATTTAGTCCACTGGATGCTTTTAACTACCGCGGTAGAAGACACCATTTGTCAGAGGCCA
CCACCCATGCCCTCTATCTGAACAACGGCAGCAACACAGCGCTCCAGCCATGAGCAGACGAGCTCCACAGCATGG
GCTCCCCCTTTCTGCTGGCGGGCTGATCGGGGGCGCGTGATTTTGTGCTGGTGGTCTTGTCTCAGCGCTTTT
GCTGGCATATGCACAAAAGGGGCGCTACACCTCCAGAAAGTGAAATACAAACCGGGGCCGGCGGAAGATGATT
ATTGCGAGGCAGGCACCAAGAAGGACAACCTCCATCTCGGAGATGACAGAAACCAAGTTTTGAGATCGTCTCCTTAA
ATAACGATCAACTCCTTAAAGGAGATTTAGACTGACAGCCCAATTACACCCCAAATGGGGGCGATTAAATACACAG
ACTGCCATATCCCAACAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGCACTGCCATACGTCAGCAGC
CAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACACACTCGTGTGTGCACATTAAGACACGCGAG
ATTACATTTGATAAATGTTACACAGATGCAATTTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAA
TGGGATTTAAAAAAAGTGCTATCTTTCTATTCAAGTTAATTAACAACAGTTTTGTAACCTCTTGTCTTTTAA
TCTT

350/550

FIGURE 350

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIPE
 GVTVLYLHNNQINNAGFPAELHNQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTISR
 AALAQLLKLEELHLDNDSISTVGVEDGAFREAISLKLFLSKNHLSSVPVGLPVDLQELRVDE
 NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPDLPGT
 HLIRLYLQDNQINHILPTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNNPWFCD
 CSIKWVTEWLKYIPSSSLNVRGEMCQGFPEQVRGMVRELNMNLLSCPTTTPGLPLFTFAPSTAS
 PTTQPPTLSIPNPSRSYPTPTTSKLPTIPDWGGRERVTPPISERIQLSIHFVNDTSIQVSW
 LSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPLDAFNRYRAV
 EDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVLLSVFCWHMH
 KKGRYTSQKWKNRGRKKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKGDRLQPIYTP
 NGGINYTDCHIPNMRYCNSSVPDLEHCHT

Important features:**Signal peptide:**

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

351/550

FIGURE 351

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCACTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA
 TGAAGAGGGCTTGCGCCGCCGGAGTAAAGAAAGAAATGACCGGGCAGCGGAGGGAGGAGCGCGCAGCGGACCGC
 GAGGGCGGGCTGCACCTCTCGAGGCTTCGAGAGTGAACCTGACACCAACATGAATTGGAGACCCATTCCAAATCTGGGACCA
 GACTTAGCGCTCTGACCGCGCTAGCGCGCGCGAGCCTCCGTGCGCGCGCGCGGGGTGGGGCTGTGCTGTGTC
 CGCGTCTCGGGCGCGCTTGGCCGTCGACAGCGGGCTGCGGGGAACCTCGGCGACCTCTGGGTGATGCGCC
 GAGCGCCATGCCCCACTACCTGCGCCTGCCTCGGGGACCTGCTGGACTCGACTCGTAAAGCGGCTAGCGCGCTCT
 CCGGAGCCACTCCGCTCTGGGTGCTGCTGGCTGGACTTAAGTCAACAAGATTAFTCTTATCAAGCAAGCACTCC
 ATGAGCGACCTTCAGAGCCTTCGAGAGTGAACCTGACACCAACATGAATTGGAGACCCATTCCAAATCTGGGACCA
 GTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAACAGGATTTGTTGAAATACTCCCTGAACATCTGAAAGAG
 TTTCACTCCCTTGAACCTTTGGACCTTAGCAGCAACAAATATTTCAGAGCTCCAACTGCATTTCCAGCCCTACAG
 CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAAATTTGGCCAAACACA
 CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTTAACTGCCCAACTGCAC
 CATCTCGAATTAAGCCGAACAGAGTAAAAATATAGATGGACTGACATTCAGGCGCTTGGTGCTCTGAAGTCT
 CTGAAATGCAAGAAATGAGTAACGAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGGAAATTTTG
 CAGCTGGACCAATAACAACTAACAGAGATTACAAAGGCTGGCTTTACGGCTTGCTGATGCTGACGAACCTTCAT
 CTCAGCGAAATGCCATCAACAGGATCAGCCCTGATGCTGGGAGTTCTGCGAGAAGCTCAGTGAGCTGGACCTA
 ACTTTCAATCACTTATCAGGTTAGATGATTCAAGCTTCTTGGGCTAAGCTTACTAAATACACTGCACATTTGG
 AACACAGAGTCAGCTACATGCTGATTGTCCTTCCGGGGCTTCCAGATTTAAAGACTTTGATCTGAAGAAC
 AATGAAATTTCTGAGCAATTGAGACATGAATGGTCTTCTCTGGGCTTGACAACTGAGCGGACATGATACCTC
 CAGGAAATCCGATCCGTTCTATTACTAAAAAGGCTTCACTGGTTTGGATGCACTTGGAGCATCTAGACCTGAGT
 GACACCGCAATCATGCTCTTACRAGGCAATGCATTTTACAAATGAAGAACTGCAACAAATGCAATTAATACAT
 TCAGCGCTTTTGTGGATTGCCAGCTAAAAATGGCTCCACAGTGGGTGGCGGAAACAACTTTTCAGAGCTTTGTA
 AATGCCAGTTGTGCCCATCTCAGCTCTAAAAAGGAAGAGCAATTTTGTGTTGATGCCAGATGGCTTTGTGTGT
 GATGATTTTCCAAACCCAGAGTACAGGTTTACGCCAGAAACACAGTCGGCAATAAAGGTTTCCAAATTTGATGTTT
 ATCTGCTCAGCTGCCAGCAGCAGTGAATCCCAATGACTTTTGGTGAAGAAACCAATGAACATCTGCATGAT
 GCTGAAATGCAAAATATGCAACCTTCCGGGCCCCAAGGTGGCGAGGTGATGGAGTATACCAACCTCTCTCGGCTG
 CGCGAGGTGGAATTTGCGAGTGGGGGAAATATCAGTGTGTCATCTCAATCACTTTGGTCTTCACTTACTCTGTC
 AAAGCCAGCTTACAGTAAATATGCTTCCCTCACTTCCAGACACCCCATGGAATCTCACCATCCGAGCTGGGGCC
 ATGGCAGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCAGATAGCTGGCAGAGGATGGGGGCACAGAC
 TCCCAGCTGCCAGGGAGAGACCATGCAATGTATGCCGAGGATGACGTGTTCTTATCTGGAATGTGAAGATA
 GAGGACATTTGGGTATATAGCTGCACAGCTCAGAACAGTCGAGGAAGTATTTCAGCAAAATGCAACTCTGACTGTC
 CTAGAAACCCCTATCTTTTGGGCCACTGTTGGACGAACTGTAACCAAGGGAGAAACAGCCCTCTCATAGCTGC
 ATTGCTGGAGGAAGCCCTCCGCCCTAACTGAACTGGACCAAAAGATGATAGCCATTTGGTGGTAACCGAGAGGAC
 TTTTGTGCGAGCGCAATCAGCTTCTGATTATTTGGGACTCAGATGTCAGTGATGCTGGGAAATACACATGTGAG
 ATGTCTGACCAACCTTTGGCAGCTGAGAGAGAAACCTGCGCCTCAGTGTGATCCCCATCCAACTCGGCAGCTCCCT
 CAGATGACAGCCCCATGCTTAGACATGACGAGTGGGCCACTGTGGGTGCTGTGATCATACCGGTGGTGTGCTGT
 GTGTTGGGCAGCTCACTCGTGGGTGGTTCATATATACCACAAAGCGGAGGAATGAAGATTTCAGCAATTACC
 AACACAGTGAACCACTTTCGACAGATATTCCTGATTTTGTCTATCTCAGGGAACCTTAGCTGACAGGCG
 GAGGGTACGTGCTTCTCAGAAAGTGGAGGCCACCAACAGTTTGTCACTCTTCAGGTGCTGATTTTCTTACCA
 CAACATGACAGTAGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGGAGCTGCCACAGATCTGTCT
 TTTTGTCCGTTTGGGATCCAGGCCCTATGTTATTTGAAGGAAATPGTATGGCTCAGATCCTTTTGAACAA
 TATCATACAGTTTGAGTCTCTGACCCAAAGACAGTTTAAATGGACCACTATGAGGCCAGTTTACATAAAGAAAGAG
 GAGTGTCTACCAATGTTCTCATCTCTCAGAAAGATCTCGGCAACGGAGCTTCAGTAAATATATCTGGGCTCTCAT
 GTGAGGAAGCTACTTAACACTATGTTACTCTCAAAATGAAGACCTGGAATGAAAAATCTGTGCTCTAAACAGCTCC
 TTTTAGATTATTAGTCAAAATCAGAGCGAGCGTGGTGGCTCGAGTAATTTCTTCACTGGGTACCTTTGGAAAT
 GCTCTCAGGAGACCTTCACTTAGATGCTTATCAAGCTTTGGACAGCCATCAGATTGTCAGCCAGAGCTTTTAT
 TGAAGAGCTCACTCTTTCCGAGCTTGGACTTGGGTGAGAGGAAGATGGGAAAGAACAGATTTTTCAGGA
 GAAATACATATTGTACCTTTAAACAGACTTTAGAAAGTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
 CATAAGACTGATGAGACCAAGGAAAGCTTAACTACTACCTCAAGTGAACCTTTATTTAAAGAGGAGAAAT
 CTATGTTTTTTAAATGGAGTTATGAAATTTAAAGAGGATAAAATGCTTTATTTACAGATGAACCAAAATTAC
 AAAAAGTTATGAAATTTTATACTGGGAATGATGCTCATATAAGAAATACCTTTTAAACTATTTTAACTTTG
 TTTATGCAAAAGAGTATCTTACGTAAATTAATGATAAAATCATGATTTTATGTTATTTTATATGCGCAGA
 TTTCTTTTATGGAATAGTATTACTAAAGCAATTTAAATAATACCTGCCTTGACATTTTATTAATAGAGGTT
 ACTTCATATATTTTGACATATATTTTAAATAAATGTCATATTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

352/550

FIGURE 352

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELQPSGVAAERPCPTTCRCIGDLLDCSRKRLARLPEPLPSW
 VARLDLSHNRLSFIRKASSMSHLSQSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVEILPEHLKEFQSLETL
 DLSNNISELQTAFFALQKLYLNSNVRVTSMEPGYFDNLANTLLVLKLNRRNISAIPEKMFKLQQLHLELNRRN
 KIKNVDLGLTFOQLGALKSLKMQNRNGVTKLMDGAFWGLSNMEILQLDHNHNLTEITKGWLYGLLMLQELHLSQNAIN
 RISPDWEEFCQKLSLDELTPHNHLSREDDSSPLGLSLNLTLLHIGNNRVSYIADCAFRGLSSLLKTLDLKNNIEISWTI
 EDMNGAFSGLDLKRRLILQGNRRISITTKAFTGLDALEHLDLSDNNAIMSLQGNAPSQMKKQLQLHLNLTSSLLCDC
 QLKWLQWVAEMNFQSPFVNSCAHPQLLKGRSIFAVSPDCFCVDDDFPKPQITVQPETQSAIKGSNLSFICSAASS
 SDSFMTFAWKKNELLHDAEMENYAHLRAGQGGVEYMTTILRLREVEFASEGKYQCQVISNHFSSSYVAKALTIN
 MLPSFTKTPMDLTIIRAGAMARLECAAVGHAPQIAWQKDGDTDFPARRERRMHVMPEDDVFTIVDVKIEDIGVYS
 CTAQNSAGSISANATLTVLETPSFLRPLDRTVTKGETAVLQCIAGGSPPKLNNWTKDDSLPVVTERHFFAAGNQ
 LLIIIVSDVSDAGKYTCESMNTLTGTERGNVRLSVIPTETCDSPQMTAPSLDDDGWATVGVVIIAVVCCVVGTSLV
 WVVIYHTRRRNEDCSITNTDETNLPAIDIPSYLSSQGTADRDQGYVSSSESGSHHQFVTSAGAGFTLPQHDSSGT
 CHIDNSSEADVEAATDLFLCPFLGSGTPMYLKGNVYSGDPFETYHTGCSDPDPTVLMDRHYEFSYIKKKECYPCSH
 PSEESCERSFSNLSWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFAANPEPASVASSNSFMGTFGKALRRPHL
 DAYSSFGQPSDCQPPAFYLYLKHSSPOLDSGSEEDGKERTDFQEENHICTFKQILENYRTPNFQSYDLDT

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

353/550

FIGURE 353

GGGGGTTAGGGAGGAAGGAATCCACCCCAACCCCTTTTCTTCTCCTTCTCGGCTTCGGACATTGG
 AGCACTAAATGAACCTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTGTTACTTTGTGATGAGATCGGGGATGA
 ATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTTGCTGGAGACGTCCTTTGTTTTGCCGCTGGAACGTTAC
 AGGGGACGCTTTCGAAGGAGAAGATCTGTCTCGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAA
 GGGCTTCACAAGTCTGACGGCTTTCAGTCCCGGACTTCCAGTTTACCATTATTCTCGATGGCAATTCCT
 CACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGGAAAAAATGGCTTGCA
 TGAATCGTTCCGGGGCTTTTCTGGGGCTGCAGCTGGTGAAGGCTGCACATCAACAACAACAGATCAAGTC
 TTTTCGAAGCAGACTTTTCTGGGGCTGGACGATCTGGAATATCTCCAGGCTGATTTTAATTATTACGAGATAT
 AGACCCGGGGGCTTCCAGGACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACC
 TGCCAACGCTGTTCCAGTATGTGCCATCACCACTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCCCTATGA
 GGAGGTCTTGGAGCAAACTCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCTTGGGACTGCACCTGTGATCT
 GCTCTCCCTGAAAGAATGGCTGGAAGAACATTCCTCAAGATGCCCTGATCGGCGGATGGTCTCGGAAGCCCCAC
 CAGACTGCGAGGTAAAGACCTTGAATGAACACCGCAACAGGACTTGTCTCTTTGAAGAACCGAGTGGATCTAG
 TCTCCCGCGCCCCCTGCCCAAGAAGAGACCTTTGTCTCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCA
 AGAGGATCATGCCACACAGGGTCTGCTCCAAACGGAGGTACAAAGATCCAGGCAACTGGCAGATCAAAATCAG
 ACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAACCCCTTAGCTAACAGTTTACCTCGCCCTGGGGGCTG
 CAGCTGCGACCATCTCCAGGGTGGGTTTAAAGATGAATGCAACAACAGGAACCTGAGCAGCTTGGCTGATTT
 GAAGCCCAAGCTCTCTAACGTGCAGGAGCTTTTCTACAGGATAACAGATCCACAGCATCCGAAATCGCACTT
 TGTGGATTACAAGAACCTCATCTCTGTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACCAACTTTCAA
 GAACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGAGAAATTCGCGGG
 GCTGCAAAACCTAGAGTACCTGAACGTGGAGTACACGCTATCCAGCTCATCTCCCGGGCCTTTCAATGCCAT
 GCCCAAACCTGAGGATCCTCATCTCAACAACAACCTGCTGAGGTCCCTGCCCTGTGGACGCTGTTCGCTGGGGTCTC
 GCTCTCTAAACTCAGCCTGCACAACAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACAGTTAACTC
 CATCATCCAGATAGACCTCCACGGAACCCCTGGGAGTGCTCTGCACAAATTGTGCTTTCAAGCAGTGGGCAGA
 ACGCTTGGGTCCGAAGTCTGATGAGCGACCTCAAGTGTGAGACGCGCGTGAACCTCTTTAGAAAGGATTTTCAT
 GCTCCTCTCCANTGACGAGATCTGCCCTCAGCTGTACGCTFAGGATCTCGCCACGTTAACTTCGCACAGTAAAA
 CAGCACTGGGTGTGGCGAGACGGGACGCATCCAACCTCTACCTAGACACAGCAGGGGTGCCATCTCGGTGTT
 GGTCCCGGACTGTGCTGTGTGTTGTGCACTCCGCCCTCACCGTGGTGGGCATGCTCGTGTTTATCCTGAGGAA
 CCGAAAGCGGTCCAAGAGACGAGATGCCAACTCTCCGCGTCCGAGATTAAATTCCTACAGACAGTCTGTGACTC
 TTCCTACTGGCAATGGGCCCTTACACGACAGATGGGGGCCACAGAGTGATGACTGTGGCTCTCACTCGCTCTC
 AGACTAAAGACCCCAACCCCAATAGGGGAGGCGAGAGGGAAGGCGATACATCCTTCCCCACCGCAGGACACCCGGG
 GGTGCAAGGGGCGTGTACCAAAATCCCGCGCCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTC
 GCACAACCGAAAGGGCTPGACCCCTTACTTAGCTCCCTCCTTGAACAAGAGCAGACTGTGGAGAGCTGGGAGA
 GCGCAGCCAGCTCGCTCTTTGTGTGAGAGCCCTTTTGACAGAAAGCCGACACGACCCCTGCTGGAAGAACTGACA
 GTGCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCGCGGGTCTATACATATATACATATATCCACATC
 TATATAGAGAGATAGATATCTATTTTCCCTGTGGATAGCCCGGTGCTGCTGTTGGCTACGCAAGGAT
 GGCAGCTGCACGAGGACATGAATGTATTGTAATAAGTAACCTTGACTTCTGAC

354/550

FIGURE 354

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFAPTQSQFYHL
FLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQTF
LGLDDLEYLQADFNLRRIDPFAFQDLNKLVLILNDNLISTLPANVFQYVPITHLDLRGNRL
KTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQGKDL
NETTEQDLCLPKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTKIPGNW
QIKIRPTAAIATGSSRNKPLANSRPCPGGCSCDHIPGSGLMKMCNNRNVSSLADLKPKLSNVQ
ELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLSRE
KFAGLQNLLEYLNVENAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSLSKLSLHNN
YFMYLPVAGVLDQLTSIIQIDLHGNPWECSCCTIVPFKQWAERLGSEVLMSDLKCETPVNFFRK
DFMLLSNDEICPOLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLLVFVT
SAFTVVGMLVFILNRKRKRDRDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHS
LSD

Important features:**Signal sequence:**

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697**N-myristoylation site.**amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

355/550

FIGURE 355

AGTCGACTGCGTCCCTGTACCCGGCGCCAGCTGTGTTCTGACCCGAGAATAACTCAGGSCTGCACCGGCCCTG
GCAGCGCTCCGCACACATTTCTGTGCGGCCCTAAGGGAACTGTTGCGCCGTGGGCCCGGGGGGATTCTTGG
CAGTTGGGGGTCGTGCGGAGCGAGGGCGGAGGGGAAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAG
GGCGGTGACCGCGCTCCAGACACAGCTCTGCGTCTCTGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC
GGGGCTCAGAGAAATGAGGCCGGCGTTGCGCCTGTGCTCTCTGCGAGGCGCTGTGCCCCGGGCGGGCGCGG
CGAACACCCCACTGCGCAGCGTGCTGGCTGCTCGGCCCTCGGGGGCTGCTACAGCCTGCACCAACCGTACCATGAA
GCGGCAGGCGGGCGGAGGAGGCTGCATCTGCGAGGTGGGGCGCTCAGCACCGTGCGTGCGGCGCGGAGCTGCG
CGCTGTGCTCGCGCTCTGCGGGCAGGCCAGGGCCCGGAGGGGCTCCAAGACCTGCTGTTCTGGGTGCGACT
GGAGCGCAGGCGTTCCCACTGCACCTGGAGAACGAGCCTTTGCGGGGTTTCTCTGGCTGTCTCCGACCCCGG
CGGTCTCGAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCAACGCTCTGCAACCGCGCGGAGATGCGCGGTACT
CCAGGCCACCGGTGGGTGCGAGCCCGAGGCTGGAAGGAGATGCGATGCCACCTGCGCGCCACAGGCTACCTGTG
CAAGTACCAGTTTGAGGTCTGTGTCTGCGCCGCGCCCGGGGCCCTCTAACTTGAGCTATCGCGCGCCCTT
CCAGCTGCACAGCGCCGCTCTGGACTTCAGTCCACCTGGGACCGAGGTAGTGCCTCTGCGGGGACAGCTCCC
GATCTCAGTTACTTGATCGCGGACGAAATCGCGCTCGCTGGGACAACTCTCGGGCGATGTGTGTGTCCTTG
CCCCGGGAGGTACCTCCGTGCTGGCAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGGCTTTGCTG
CGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACAGTGGGGAAGGACAGCCGACCT
TGGGGGGACCGGGTCCCCACAGGCGCCGCGGCCACTGCAACACGCCCCGTGCGCGAGAGAATGCGCAAT
CAGGGTCGACGAGAAGCTGGGAGAGACCACTTGTCCCTGAACAAGACAATTAGTAACATCTATTCCTGAGAT
TCTTCGATGGGGAACACAGAGCACGATGTCTACCTTCAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCAC
CCCATCAGGAGCGTGATTTCCAGTTTAAATCTACGACTTCTCTGCCACTCCTCAGGCTTTCGACTCCTCCTC
TGCCTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCTTGACCATGACAGTACTGGGCTTGT
CAAGCTCTGCTTTCCAGAAAGCCCCCTCTCCAGCCAAGGAAGGAGTCTATGGGCCCGCGGGCTGGAGAGTGA
TCTTGAGCCCGCTGCTTTGGGCTCCAGTTCGACATTGCACAACAATGGGGTGAAAGTCGGGGACTGTGATCT
GCGGGACAGAGCAGAGGCTGCTTGTGCGGAGTCCCTCTTGCTCTAGTGATGCATAGGAAACAGGGGACA
TGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAACGGGGAACCAAGAGGAACCTACTGTGTAACGTACAA
TTTCTGCAGAAATCCCCCTTCTCTAAATCCCTTTACTCCACTGAGGAGCTAAATCAGAATGCACACTCCTTC
CCTGATGATAGAGGAAGTGAAGTGCCCTTAGGATGGTGATACTGGGGGACCGGAGTAGTGCTGGGAGAGATATT
TCTTATGTTTATTCGSAGAATTTGGAGAAGTGATTGAACTTTCAAGACATTGSAACAAATAGAACACAATAT
AATTTCATTAATAAATAATTCTACAAATGGAAGGAATGTTCTATGTTGTACGGCTAGGAGTATATTGG
TTCGAAATCCGAGGAAAAAATAAAAAATAAAAAATTAAGGATTGTTGAT

356/550

FIGURE 356

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGA¹ST
VRAGAELRAVLALLRAGPGPGGGSKD²LLFWVALERRRSHTLENEPLRGFSWLSSDPGGLES³D
TLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPPAPRPGAASN
LSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPGRYLR
AGKCAELPNCLDDLGGFACECATGFELGKDGRCVSTSGEGQPTLGGTGVPTRRPPATATSPVP
QRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVIS
KENSTTSSATPQAFDSSSAVVFI⁴FVSTAVVVLVILMTVLGLVKLCFHES⁵PSSQPRKESMGPP
GLES⁶DP⁷EP⁸AALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Important features:**Signal sequence:**

amino acids 1-16.

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

357/550

FIGURE 357

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTGCTCTCTTCAACCAGACCTCTACATTTCCATTTTGGGAAGA
AGACTAAAATATGGTGTTCCTCAATGTGGACACTGAAGAGCAAAATTCCTATCCCTTTTAAACATAATCCTAATTTCC
AAACTCTTTGGGGCTAGATGGTTCTCTAAACTCTGCCCTGTGATGTCACTCTGGAGTCTTCCAAAGAACATATGTG
ATCGTGGACTGCACAGACAGCAATTTGACAGAAATTCCTGGAGGTATTCCCAAGAACACCCAGACCTTACCCTC
ACCATTAACCCACATACCAACATCTCCCCAGCGCTCTTCACAGACTGGACCATCTGGTGTAGAGATCGATTTTCAGA
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAACCAACATGTGCATCAAGAGGCTGCAGATTTAAACCCAGAAGC
TTTAGTGGACTCACTATTAAAAATCCCTTTACCTGGAGTGGAAACACAGCTACTAGAGATACCGCAGGGCTCCCG
CCTAGCTTACAGCTCTCAGCGCTTGAGGCCAACCAACATCTTTCCATCAGAAAAGAGAACTTACACAGAACTGGCC
AACATAGAAATACTCTACCTGGGGCCAAACTGTTATTATCGAAATCCTTGTATTGTTTCATATTCAATAGAGAAA
GATGCCCTTCCATAACTTGACAAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAACTGCACAGCCGCTCCCTACTGTT
TTGCCATCTACTTTAACAGAACTATATCTCTACAAACAACTGATTGCAAAAATCCAAAGAAATGATTTTAATAAC
CTCAACCAATTACAAATTCCTTGACCTAAGTGGAAATTGCCCTCGTGTATTATAATGCCCAATTTCTTGTGGCGCG
TGTAATAATAATTTCTCCCTACAGATCCCTGTAATGCTTTTGTAGGCGCTGACAGAAATAAAAGTTTACGTCTA
CACAGTAACCTCTCTCAGCATGTGCCCCAAAGATGGTTTAAAGAACTCAACAACCTCCAGGAATCGGATCTGTCC
CAAACTCTCTGGCCAAAGAAATTTGGGAGATGCTAAATTTCTGCATTTCTCCCCAGCACTCATCCAAATGGATCTGT
TCTTTCAATTTGAACCTTCAGGCTCATGTGCATCTATGAATCTATCAAGCAATTTCTTCACTGAAAAGCGCTG
AAAATTCCTGGGATCAGAGGATGTGCTTTTAAAGAGTTGAAAAGCTTTAACTCTCGCCATTACATAATCTTCAA
AATCTTGAAGTTCCTGATCTTTGGCACTAACTTTATAAAAATTGCTAACTCAGCATGTTTAAACAAATTTAAAAGA
CTGAAAGTCATAGATCTTTCAAGTAATAAATATCACTTCAGGAGATTCAAGTGAAGTTGGCTTCTGTCTCAAAT
GCCAGAACTCTGTAGAAAGTTATGAACCCAGGCTCTGGAACAAATACATTTATTCAGATATGATAAGTATGCA
AGGAGTTGCAGATTCAAAAACAAAGAGGCTCTTTTCATGTCTGTTAATGAAAGCTGCTACAGATATGGGACAGC
TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTCAGCATCTTTCTTTCTCAAATGCGCTG
AATCTGTCAAGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATTCACAACTTTAGCAGAGCTGAGATATTG
GACTCTCTCAACACCCGGCTTGATTTCACTCCATTCAACAGCATTTGAAGAGCTTCACAAATCGGAAGTTCTGGAT
ATAAGCAGTAATAGCCATTTATTTCACTCAGAGGAATTACTCATATGCTAACTTTACCAAGAACTCAAGGTT
CTGCAGAACTGATGATCAACGCAATGACATCTCTTCTCCACAGCAGGACCATGGAAGAGTGAGTCTCTTAGA
ACTCTGGAATTCAGAGAAATCACTTAGATGTTTATGAGAGAGAGGTGATAACAGATACTTACAATTTATTCAG
AATCTCTAAAATTAGAGGAATTAGACATCTCTAAAATTTCCCTAAGTTTCTTGCCTCTGGAGTTTGTATGGT
ATGCCCTCAAATCTAAAGAATCTCTCTTTGGCCAAAATGGGCTCAAATCTTTCAGTTGGAGAGAACTCCAGTGT
CTAAAGAACCTCGGAACTTTGGACCTCAGCCACAACCACTGACCCTGTCCCTGAGAGATTATCCAACTGTTCC
AGAAGCTCAAGAACTCTGATTCTTAAGAATAATCAAATCAGGAGCTGACGAAGTATTTTCTCAAGATGCTCTC
CAGTTGCGATATCTGGATCTCAGCTCAGCTAATAAATCCAGATGATCCAAAGACCACTCTCCCAAAAATGTCTC
AACAACTCTGAAGATGTGCTTTGTCATATAATCGGTTTCTGTGCACCTGTGTGCTGTGTGGTTTGTCTGGTGG
GTTAACCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGACACACAAGGGC
CAAGGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACTGTGATCTGTTTCTCAATTTCCATA
TCTGTATCTCTCTTTCTCATGTGTGATGATGACAGCAAGTCACTCTATTCTTGGGATGTGPGTATATTACCAT
TTCTGTAAAGCCAAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATCTGTAT
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTGGCTGAGCTGTGGCCAACTGGAGAGCCCAAGAGGAA
CATTTTAATTTATGTTCTCAGGGAAGGGACTGGTTACAGGGCAGCCAGTCTTGGAAAACCTTTCCACAGCATCA
CAGCTTAGCAAAAAGCAGGTGTTTGTGATGACAGCAAGTATGCAAGAGCTGAAAATTTTAAAGATGACATTTTAC
TTTTPCCATTCAGAGGCTCATGGATGAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAAGCCCTTTCAGAG
TCCAAGTTCTCTCCAGCTCCGGAAAAAGGCTCTGTGGGAGTTCTGTCTTGTGAGTGGCCACAACCCCGCAGCTCAC
CCATACCTCTGCGAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCTCTATGTCAGGTGTTCAAGGAA
ACGGTCTAGCCCTTCTTGCAAAACACAACTGCCTAGTTTACCAAGGAGAGGCTGGC

358/550

FIGURE 358

MVFPMTLKRQILILFNIIISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGGI
PTNTNTLTLTINHIPDISPASFHRLDHLVEIDFRNCNCPVPLGSKNNMCIKRLQIKPRSFSGL
TYLKSILYLDGNQLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYYRNP
YVSYSIEKDAFLNLTCLKVLSLKDNNTAVPTVLPSTLTLEYLYNNMIAKIQEDDFNNLNQLQ
ILDLSGNCPCRYNAPFPAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWFKNINK
LQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSNFELQVYRASMNSQAFSSLSKLTIRIR
GYVFKEKLSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVKNISP
SGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTL
DLSKNSIFFVKSSDFQHLSEFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFEELHKEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKMMNDNDISSSTSRTESESL
RTLFEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLS
LAKNGLKSFSWKKLQCLKNLETDLSHNQLTTPPERLSNCSRSLSKNLILKNNQIRSLTKY
FLQDAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTDAVWVFWVWNHTEV
TIPYLATDVTGVPGAHKQGSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLY
FWDVWYIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKH
FNLCLEERDWLPQGPFVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEK
VDVIIIFLEKPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNH
VAYSQVFKETV

Important features:**Signal sequence:**

amino acids 1-26

Transmembrane domain:

amino acids 840-860

359/550

FIGURE 359

GACGGCTGGCCACC**ATG**CACGGCTCCTGCAGTTTCTGTATGCTTCTGCTGCCGCTACTGCTAC
TGCTGCTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGTATGTTGG
AGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGAGAT
GGGACGAGGAGCTGGCCGCCCTTCGCCAAGGCTACGCACGGCAGTGCGTGTGGGGCCACAACA
AGGAGCGCGGGCGCCGCGCGGAGAACTCTGTTGCCATCAGACGAGGGCATGGACGTGCCGC
TGGCCATGGAGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGCAGCC
CAGGGCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATCGGCTGTG
GTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACTGGTGTGCA
ACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTCCGTGCTCCC
AATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGCCCGGAAGATG
CTCAGGATTTGCCTTACCTGTTAACTGAGGCCCCATCCTTCCGGGCGACTGAAGCATCAGACT
CTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCTTGGTAACAGAGG
TCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCCCCAACTTCTTAG
CAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAACAACATGAGGTCCCTT
CCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTACCTTCCCCAAATCGA
CCCATGTTCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACAAAAGTGCCCTCTAGGA
GCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAGGGAACCTCCTACCCCATG
CCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCTTCCAGTGAGGTCTTGGCCTCAGTTT
TTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGACCACACGGGGCACACCTCCT
CCAAGTCCCTGCCCCAATTTCCCCAATACCTCTGCCACC GGCTAATGCCACGGGTGGGCGTGCCC
TGGCTCTGCAGTCGTCCTTGCCAGGTGCAGAGGGCCCTGACAAGCCTAGCGTTGTGTAGGGC
TGAATCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGACTACTGCTCCTGCCTCCTCTGG
TGTTGGCTGGAATCTT**TGA**ATGGGATACCCTCAAAGGGTGAAGAGGTGAGCTGTCTCCTCTG
TCATCTTCCCCACCTGTCCCCAGCCCCATAACAAGATACTTCTTGGTTAAGGCCCTCCGGAA
GGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCCATCTGGAGGCACAAGGCCCTGGCTG
GCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACCGGGCCACACCTCTCCTGCCCTCCC
TCCTGAGTCTCGGGGTGGGAGGATTTGAGGGAGCTCACTGCCTACCTGGCCTGGGGCTGTCT
GCCCACACAGCATGTGCGCTCTCCCTGAGTGCCTGTGTAGCTGGGGATGGGGATTCTAGGGG
CAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCTTTGAGTGGGGGAGGCAGGGACGAGGGAA
GGAAAGTAACCTCGACTCTCCAATAAAAAACCTGTCCAACCTGTGAAA

360/550

FIGURE 360

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPASDMLHMRWDEEL
AAFAKAYARQCQVWGHNKERRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMC
GHYTQVWAKTERIGCGSHFCEKLGVEETNIELLVLCNYEPPGNVKGKRPYQEGTPCSQCPSG
YHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTSPSSLATGIPAFVLVTEVSGSL
ATKALPAVETQAPTSLATKDPSPMATEAPPCVTTTEVPSILAAHSLPSLDEEPVTFPKSTHVPI
PKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLASVFPAQD
KPGELQATLDHTGHTSSKSLPNFPNTSATA¹NATGGRALALQSSSLPGAEGPDKPSVVVSGLNSGP
GHVWGPELLGLLLPLVLVLAGIF

Important features:**Signal sequence:**

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

361/550

FIGURE 361

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGAGCCGGCAGGGAGCGAACCAGGACTGG
GGTGACGGCAGGGCAGGGGGCGCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAACT
GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACTGCG
AGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCT**ATg**AGGCCACTCCTCGTCTGCTGCT
CCTGGGCGCTGGCGGCCGGCTCGCCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCCCGG
GCACCCCGGCGCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCGCGATGG
CCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGAGGCCGGG
ACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGGCGGGACCCGCGGGGCCACCGG
GCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCG
GGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACA
TTACGACGCCGTCAACGGCAAGTTACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCA
TGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTC
TTTCTCCAGTTTTTTCGGGGGGTGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGGTGAG
GCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGC
CAGCATCAAGACAGACAGCACCTTCTCCGATTTCTGGTGTACTCCGACTGGCACAGCTCCCC
AGTCTTTGCT**TAG**TGCCCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGGTGTGA
GGCTGACAACAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGGAGG
TGGGGTAGAGCACTCTCCGTCTGCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCA
GGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAGACCAGAGGAGTGTGCTGTGCTGG
CAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTCCTGGTC
CTCTGCTTCTCTGGATCTCCCCACCCCTCCTGCTCTGGGGCGGGCCTTTTCTCAGAGAT
CACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

362/550

FIGURE 362

MRPLLVL LLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPG
EKGEGRPGLEPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLEFD
RVLVNEQGGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPA
SLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSWDWHSSPVFA

Important features:**Signal sequence.**

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

364/550

FIGURE 364

MMWRPVSLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGRE
VAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDTYD
TDRDGRVGWEEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSDMATREELT
AFLHPPEEFPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEEPAAWVQTERQQFRDF
RDLNKDGHLDGSEVGHWWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFVGSQAT
NYGEDLTRHHDEL

Important features:**Signal sequence:**

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302**N-myristoylation site.**

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

365/550

FIGURE 365

GTCCTGTTCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGCCCTGATCGCG**ATG**GGGACAAAG
GCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGGCA
TTGGGCAAGTGTACAGTGCACCTCTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCTGTG
AAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGA
GACACCACCAGACTCGTTTGTCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACC
TTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACTGGGACATACACTTGT
ATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTG
CCTCCATCCAAGCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGGCAGTGCTG
ACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTG
ATGCCCTACGAATCCAAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCTGAATCCACACA
ACAGGAGAGCTGGTCTTTGATCCCCGTGCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCA
CGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT
GTGGGGGTCTCGTGGCAGCCGCTCCTTGTAACCCGTGATTCTCCTGGGAATCTTGGTTTTTGGC
ATCTGGTTTGCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGACTTCGAGTAAGAAG
GTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTG
GTG**TGA**GCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACT
CTGGCCCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTCTACACCCACAGGGCCC
CCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTC
CCTCCCTTCCTACCCTGCTGAGTGGCCTGGAACCTTGTTTAAAGTGTTTATTCCCCATTCT
TTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAA
TGGCGGGGGTCGAGGAATCTGCACTCAACTGCCACCTGGCTGGCAGGGATCTTTGAATAGG
TATCTTGAGCTTGGTTCTGGGCTCTTTCTTGTGTACTGACGACCAGGGCCAGCTGTTCTAGA
GCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGGTCTTCCAT
CTCTGGGGCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCCCTCTGCCCTGTC
CTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAAATGGGAGCTTGTGTGTGGA
GAGCATAGTAAATTTTACAGAACTTGAAGCCAAAAGGATTTAAACCGCTGCTCTAAAGAAA
AGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCAGAGGCTGAGGCAGGCGGAT
CACCTGAGGTGCGGAGTTTCGGGATCAGCCTGACCAACATGGAGAAACCCCTACTGGAAATACAA
AGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCCAGCTGCTCAGGAGCCTGGCAACAAGAG
CAAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

366/550

FIGURE 366

MGTKAQVERKLLCLFILAILLLCSLALGSVTVHSSEPEVRI PENNPVKLSCAYSGFSSPRVEWK
FDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGT YTCMVSEEGGNSYGEVKVKL
IVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNSSYV
LNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVTLLLLGI
LVFGIWFAYSRRGHFDR TKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

367/550

FIGURE 367

GGGGAGAGGAATTGACCATTGAAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCCTTGCRAAAATG
 AAGGATGCGAGGACCGCAGCTTTCTCCTGGAAACCGAACGCAATGGATFAAACTGATTGTGCAAGAGAGAAAGGAAC
 GAAGCTTTTTCTTTGGAGCCCTGGATCTTAACACAAATGTGTATATCTGCACACAGGAGGACCTCAAGAATAGAAA
 TAAACCAAGAGTTAGACCCCGGGGGGTGGTGTGTTCTGACATAAAATAAATACTTAAAGAGAGCTGTTCCCTCC
 CCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCAACAAGAAAAAGATGTTCATTCTTCTC
 TATAAAGAGAAAGTGAACCAAGGAGATATTTTGAATGAAAAGTTTGGGGCTTTTTTACTAAGTAAGAAGACT
 GGTGGTGGTGGTGGTCTTCTTCTTTTTGAATTTCCACAAAGAGGAGGAAATTAATAATACATCTGCARAGAAA
 TTTCAGACAGAAAAAGTTGACCCGCGCAGATTGAGGCATTGATTGGGGAGAGAAACAGCAGAGACAGTTGGA
 TTTGTGCCATGTTGACATAAAATGACGGATAATGCAAGTTGERTTTTTCTCATCAACCTCCTTTTTTTAAAT
 TTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTTAACCACTGGGATTTCCATCTGGATGTGCT
 GTGATCAGTCTGAAATACAACCTGTTGAATTCAGAGGACCAACACCGATATAATTTGAAATGTTGAACAGAT
 GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTTGACCCCTGCTTGTGGTGGCT
 GCTGGCTCTTCAACTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGACGAA
 CCAAGTTCAAGCAAGGTGATTTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT
 GCTGAACCTCCATGAGAACCAATCCAGATCATCAAATGAACAGCTTCAAGCACTGAGGCATTTGGAATCCT
 ACAGTTGAGTAGGAACCATATCAGAACCATTTGAAATTTGGGGCTTTCAATGGCTGGGCACCTCAACACTCTGGA
 ACTCTTTGACAACTCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAACTGAAGGAGCTCTGGT
 GCGAAACACCCCATTTGAAGCATCCCTCTTATGCTTTTAAACAGAAATCCTTCTTTGCGCCGACTGACTTAGG
 GGAATGAAAAGACTTTATACATCTCAGAGGTGGCTTTGAAGGTCTGTCCAACTGAGGATTTGAACCTTGC
 CATGTGCAACCTTCGGGAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA
 TTTATCTGCCATCAGGCTGGCTCTTCCAGGTTTGTATGCACCTTCAAAAACTGTGGATGATACAGTCCAGAT
 TCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGGCACAAATATCTAAC
 ATTAAGTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACATTTACATCAACAACCTTGGAACTG
 TAACTGTGACATCTGTGGCTCAGCTGGTGGATAAAGACATGGGCCCCCTCGAACACAGCTTGTGTGGCCCGGTG
 TAACTCTCTCCCAATCAAAGGGGAGGTACATTGGAGAGCTCGACCAAGATTACTTACATGCTATGCTCCGGT
 GATTGTGGAGCCCTCCAGACCTCAATGTCACTGAAGGATGGCAGCTGAGCTGAAATGTCGGGGCTCCACATC
 CTCGACATCTGATCTTGGATTACTCPAATGGAACAGTCATGACACATGGGGCGCTACAAGTCCGGATAGCTGT
 CCTCAGTGTGTGACGTTAAATTTCAAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTCAGTAA
 TTCGGTTGGGAATACTACTGCTTCAGGCACCCCTGAATGTTACTGCAGCAACCATCTACTCCTTCTTACTTTTC
 AACCGTCACAGTAGAGACTATGGAAACCGTCTCAGGATGAGGCACGGACCCAGATACAATGTGGGTGCCACTCC
 AGTGTCCGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCAACAGAGCAAGGTGCAGAGAGAAAACTT
 CACCATCCCCAGTGACTGATATAAACCAGTGGGATCCAGGAATGTATGAGGTCTATGAAGACTACAAAATCATCAT
 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGAATGCTGGTCACTTTTCTACAAGATGAGGAAGCAGCACC
 TCGGCAAAACCATCAGCCCCAACAGGACTGTTGAAATTTATTAATGTGGATGATGAGATTACGGGAGACACACC
 CATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
 CAACCAACCAACACAGTTTAAACACATAAATTCATACACAGTTCACTGATGAACCGTTATTGATCCGAATGAA
 CTCTAAAGCAATGTACAAGAGACTCAATCTAAACACTTTACAGAGTTACAAAAAGCAACATCAAAAAAAA
 GACAGTTTTATTAATATGACCAAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGCTTTACAAAAAACAA
 AAAAGAAAAAATTTTATTATAAAATTCATTGTGATCTAAAGCAGCAAAA

368/550

FIGURE 368

MLNKM TLHPQQIMIGPFRNRLFDPLLVL LALQLLVVAGLVRAQTCPSVCSNQFSKVICVRKNLREVPDGIS
TNRLLNLNHNQIQI IKVNSFKHLRHLLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKL
KEILWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFGLSNLRYLNLAMCNLREIPNLTPLIKLDLDEL
LSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH
NPWNCNCDI LWSWIKDMAPSNTACCA RCNTPPNLKGRI GELDQNYFTCYAPVIVEPPADLNVT EGMAAELKC
RASTSLTSVSWITPNGTVMTHGAYKVRIAVLS DGTLNFTNVT VQDTGMYTCMVNSVGN TTASATLNVTAAT TTP
FSYFSTVTVETMEPSQDEARTDNNVGP TPVVWDETTNTVITSLTPQSTRST EKTFTTIPVTDINS GIPGIDEVMKT
TKI IIGCFVAITLMAAVMLVIFYKMRKQHHRQNHAPTRTVEI INVDD EITGDTPMESHLPMPAIEH EHLNHNYS
YKSPFNHTT VNTINSIHSSVHEP LLIRMN SKDNVQETQI

Important features:**Signal sequence:**

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446,
488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397,
422-428, 433-439, 531-537

369/550

FIGURE 369

CAAAACTTGGCTCGCGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCGAGCCGCGGAGCGCAGCTGAGAC
 TGGGGGAGCGCGCTTCGGCCTCTGGGGCGCCGCTCGGGCGCCGGGGCGAGCAGGGAAGGGGAAGCTGTGGTCTGCC
 CTGTCTCCAGCAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCGCTCCCTATCCCTCTTTATATA
 GAAACCTTCCACACTGGGAAGGCGAGCGGCGAGGCGAGGAGGGCTCATGGTGGAGCAGGAGGCGCGCTGATCTGAGC
 GCGCAGAGCATCCGAGTTTACAGATTTTACAGATACCAATGGGAAGGCGAGGAGGCGAGACAGCTGCTCGTGGT
 TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTCGACGCAACCATGGCCCCAGCGCGGCTGTGC
 TGCTCTGTCTGTCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGGCTGTGGGGCCCGAGGATTTGGCCGAA
 CTGGCGCCACAGCGCTGAGCCGCCGAAGAGAAGCAATTTGCGGAGGAGGAGCCGCTGCTGGTACTGAGCCTTGAGG
 AGCCCGGGGCTGGCCAGCGCGGCTGAGCTGCCCCGAGACTGTGCTGTTCCGAGGAGGGCGTGTGGACTGTG
 GCGGTATTGACCTGCGTGAGTTCOCGGGGGACCTGGCTGAGCACACCAACCACTATCTCTGCAGAACAACGAGC
 TGGAAAAGATCTACCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA
 CTTCCCGAGGGCTCCAGAGAAGCGTTTGAAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAAATAACAAGC
 TGACCTTGGCACCCGCTTCTGCCAAACGCGCTGATCAGTGTGGACTTGTCTGCCAATATCTACCAAGATCT
 ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGAGCGCGGGC
 TGGCGGACAACATGTTCACGGGCTGCAGCAACGTCGAGGTCCTCATCTGTCCAGGACATTTCTGGCCAGGCTGC
 CCAAGCACCTGCCGCTGCCCTGTACAAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGCGGGCCT
 TCAGCGAGCTGAGCAGCCTGCCGAGCTATACCTGCAGAACAACCTACCTGACTGACGAGGGCCTGGACAACGAGA
 CTTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC
 CGCGCAGCCTTGGTGTCTGCTGATCTGGAGAAGAAGCCATCCGGAGCGTGGACGCCAATGTGCTGACCCCATCC
 GCAGCCTGGAGTACCTGTCTGTGCACAGCAACAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC
 TCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTGCACATGGCCCTGCCTGCGCCGCTGC
 GCACCTCATGTATCCTGCACAACAGATCACAGGCTTGGCGCGGAAGACTTTGCCACCACTACTTCTCTGGAGG
 AGCTCAACCTCAGCTACAAACGCATCACCAGCCACAGGTGACCGCGAGCGCTTCCGCAAGCTGGCGCTGTGC
 TCTCGCTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCATCGAAATGTCCATGTGCTGAAGG
 TCAAGCGCAATGAGTGTGCTGCTTGGCAGAGGGGCGCTGGCGGCGCATGGCTCAGCTGCGTGAGCTGTACATCA
 CCAGCAACCGATGCGCAGCGAGCCCTGGGCCCCGCTGCTGGTGGACTGCCCATCTGCAGCTCTGTGGACA
 TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTGAGTACCTGTACTGCAGAACAACA
 ACATTAGTGGCGTGGCCGCCAATGCTCTCGACTCCAGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAAACAAGC
 TGGCTGTGGGCTCCGTGTGGAGAGTGCTTCCGGAGGCTGAAGCACTCTGAGGTCTTGGACATTGAAGGCAACT
 TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
 AGGAAGAGGAAACAAGATAGTGACAAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCGGACTCTTTTCTGC
 AGCACAGCCTGTGTGCTGTGAGGCCCCCACTCTGCGGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
 TCCACATGACACGGGCTGCACAGTCTCATATCCCAACCCCTTCCCACGGCGTGTCCACGGCCAGACACATGC
 ACACACATCACACCTTCAACACCCAGCTCAGCCACACACAACCTACCTCCAAACACCAACAGCTCTGTGCACAC
 CCCCACATACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGCTCTGCCCTGCCCTGGCACACACAGGCAACCA
 TCTCCCTCCCTGCTGCATGTGTATGCGGTATGCATACACAGGACACACACATGCAAGTCAATGTGTGGGA
 CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTTGGCCAGCCAGAAATCAGCCATAGCAGCTTSCCGTCTGCCCT
 GTCCATCTGTCCGTCGTTCTTCTGGGAAGACACAAGGCTATCCATGCTCTGTGGCCAGGTCCTGCCACCTCT
 GGAATCCACAAGAGCTGGCTTTTATCTTTCCATCCGATTTGGGGACAGGAGCCTCAGGAGCTGCTGGCTGGCC
 TGGCCCACTGCTCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCTCTGGCAGGACA
 CAGCAGCTTTTCCATGGGCAAGCCAGTGAAGGACAGGATGGGAGAGCCCTGCTGGGCTGCTGGGCTGGG
 GAGGCTGAAGCAGAGGTGATGGGGCTGGGCTGAGGCCAGGAGGAGGACCCAGCTGCACCTAGGAGACACCTTT
 CTGCTTCCGGCTGTGGGGGAAGTTCGGGTCCTTTATTTTATCTTTTAAAGGAAAAAATGATAAAAAAT
 CTCAAAGCTGATTTTCTGTATAGAAAACCTAATATAAAGCATATATCCCTATCCCTGCAAAAAA

370/550

FIGURE 370

MEGEEAEQPAWFHQPWRGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRSG
GHSLSPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCCGGIDLREFPGDLPEH
TNHLSLQNNQLEKIIYPEELSRHLRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNKLT
APRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNVEVLI
LSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDGLDNETFWK
LSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLHNSQLREQG
IHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYFLEELNLS
YNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALARGALAGMA
QLRELYLTSNRLRSRALGPRAWDLAHLQLLDIAGNQLTEIPEGLPESLEYLYLQNNKISAVP
ANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGLGKEKEE
EEEEEEEEETR

Important features:**Signal sequence:**

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554**Leucine zipper pattern.**amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

371/550

FIGURE 371

CACITTTCTCCCTCTCTTCCCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGACCTCGGAGACCGCG
 CCGGGGAGACCGGAGTGCTGTGGTGGGGGGGACCTGTGGCTGCTCTGACCGCCCCACCCCTCTCTTCTGCGAC
 TGGCGTCTCTCCGGAAGACCTTTTCCCTGCTCTGTTTCTTACCGAGTCTGTGCGATCGCCCCGGACCTGGCCGG
 GAGGAGCTGTGGCCGGCGGGAGATGCTTAGGGGGCGGGCGGGAGGAGCGGGCGGGGACGGAGGGCCGGGAG
 GAAGATGGGCTCCCTGGACAGGGACTCTTGTGGCGTACTGCTGCTCCCTTGCCCTTTGCCCTCTGGCTGGTCTT
 GAGTCTGTGCCCCATGTCCAGGGGGAAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGCCCTGCCCTGGCCAGCA
 TGCCGAGAGGGCTGAAGAACAACATGAAAATAACAGGCCAGTCAGGACCAAGGGGCTCCCTGCTTCCCGTGCTT
 GCGCTGCTGTGACCCCGGTACTCCATGTACCCGGGACCGCGCTGCCCCAGATCAACATCACTATCTTGAAGG
 GGAGAGGGGTGACCCGCGAGATCGAGGCTCCAAAGGGAATATGCGAAAACAGGCTCAGCAGGGGCGAGGGGCCA
 CACTGGACCCAAAGGGCAGAGGGGCTCCATGGGGGCCCTTGGGAGCGGTTCAAGAGCCACTACGCCGCTTTTC
 GGTGGGCGGAAGAAGCCCTGACAGCAACCACTACTACAGACGGTGTATCTTGACACGGAGTTCGTGAACCT
 CTACGACCACTTCAACATGTTCAACGGCAAGTTCTACTGCTAGCTGCCCGGCTCTACTTCTTCAAGCTCAACGT
 GCACACCTGGAACCGAGAGAGCTTACCTGCACATCATGAAGAACGAGGAGGAGGTGGTGTATCTTGTTCGCGCA
 GGTGGGCGACCCGACGATCATGCAAGCCAGAGCTGATGCTGGAGCTGCGAGAGCAGGACCAAGTGTGGGTACG
 CCTCTACAGGGCGCAAGTGAAGAACCCATCTTCAAGGAGGAGCTGGACACCTACATCACTTCACTGGGTACCT
 GGTCAAGCAGCCACCGAGGCCCTAGCTGGCGGCCACCTCTTCTCTCGCCACCTTCCACCCCTGGGCTGTGC
 TGACCCACCGCTCTTCCCGATCCCTGGACTCCGACTCCCTGGCTTTGGCATTCACTGAGACGCCCTGCACAC
 ACAGAAAGCCAAAGCGATCGGTGCTCCAGATCCCGCAGGCTCTGGAGAGAGCTGACCGCAGATGAATCAACCA
 GCGCGGCGACCCGCGAGAAACCTTCCGGACCTTCCGGGCGCTCTCTGCACACATCTCAAGTGACCCCGCAGG
 CGAGACCGGGGTGGCGGCGAGGCGTCCAGGGTGGCGCACCGCGGCTCCAGTCTCTGGAATATATAGGCAAAAT
 CTAAGGCTCTCAAAAGGAGCAAGTAAACCGTGGAGGACAAGAAAAGGTTGTTATTTTCTCTTCCAGCCAG
 CCTGCTGGCTCCAAAGAGAGAGGCTTTTCACTGTGAGACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGG
 GTCAGGGGAGGGGCGGGGGCAGGAACTACCTCTGGCTTAATCTTTTAAAGCCAGTAGGAACCTTTCTTGAAGG
 ATAGGTGGACCTGACATCCCTGTGGCTTGCCTCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGTGA
 TGGGGGCTGGGGCCCCAGGCTCAGCTCCAGAGGGACAGCTGAGCCCTGCTTGGCTCCAGGTTGGTAGAA
 GCACCGCAAGGGCTCTTCAAGTGGCGAGGACCCCTGGGTCCCCAGGCTCGAGATGTTCTATAGGGGGAG
 AGCTCTTGGTACATCTCATGTGTGCTCTGCTTCCACCCCTGTGCCACCCAGAGCCTGGGGGGTGGTCTTCCATG
 CCTGCCACCTGGCATCGGCTTCTGTGCCGCTTCCACACAAATCAGCCCCAGAGGCCCCGGGGCTTGGCTT
 CTGTTTTTTATAAAACACCTCAAGCAGCACTGCACTCTCCATCTCTCTGTTGGGCTAAGCATCACCCTTCCAG
 TGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCOCTCATCCAGGCTCTGACCA
 GTAGCCTGAGAGGCGCTTTTCTAGGCTTCAAGCAGGGGAGAGCTGGAAGGGGCTAGAAAGCTCCCGCTTGTCT
 GTTCTCAGGCTCTGTGAGCTCAGTCTCAGACAGAGTCAAGAGGAATACAGCTCCCAATCAACCGTGTCA
 GGATCACTCTCAGGAGCTGGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATTCAGGACCAAGCTGGAGCAGGG
 TTGGGTGTCTCCACGGTGCTCTCGCCCTGCCATGGCCACCCAGACITGATCTCCAGGAACCCCATAGCCCC
 TCTCCACCTCACCCCATTTGATGCCCCAGGGTCACTCTTGCTACCCGCTGGGGCCCCCAACCCCGCTGCTCTC
 TTCCTTCCCCCATCCCCACCTGGTTTGAATCAATCTGCTTCCCTCTCTGCGGCTGAGACTCTGAAGCCGAGTGTCTGTGGGGTGGCCGGAAG
 TCCCTAAGTCCCTCTCTTTAAAGAACTTCTGCGGGTCAAGTCTGAAGCCGAGTGTCTGTGGGGTGGCCGGAAG
 CAGAGGGCCCACTCGCTGCTTAAGCTCCCCAGCTCTTCCAGAAAACATTAAACTCAGAATGTGTTTTCAA

372/550

FIGURE 372

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELFSPPDHAERAEQHEKYRPS
QDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQKYGKTSAGARGHTG
PKGQKGSMPGERCKSHYAAFVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFYCYV
PGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGD RSIMQSQSLMLELREQDQVWVRLYK
GERENAI FSEELDTYITFSGYLVKHATEP

Important features:**Signal sequence.**

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

373/550

FIGURE 373

CGGAGTGGTGCGCCAACGTGAGAGGAAACCGTGC GCGGCTGCGCTTTCCTGTCCCCAAGCCG
TTCTAGACGCGGGAAAAATGCTTTTCTGAAAGCAGCTCCTTTTGAAGGGTGTGATGCTTTGGAA
GCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAATAGAATGC
ACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTAGAGG
ATGAGCGCATGGAGCTCAGTAAGAGCTTTTCGAGTATACTGTATTATCCTTGTAAAACCCAAAG
ATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAGAGTTCT
TCAGTCTGAAAATGTTAAAGTGTTGAGTCAATTAATATGGACACAAATGACATGTGGTTAA
TGATGAGAAAAGCTTACAAATACGCCCTTTGATAAGTATAGAGACCAATACAACCTGGTTCTTCC
TTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAAAAAAGGATC
CATCAGAGCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATATGTGGGTATGG
AAGGAGGAATTGTCTTAAAGTGTAGAATCAATGAAAAGACTTAAACAGCCTTCTCAATATCCCAG
AAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAACAGCTAGCAGTTT
GCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGAAGATGTATTTA
ATACCAAATCTGTGGGCTTTCTATTAAAGAGGCAATGACTTATACCCCAACAGGTAAGTAG
AAGGCTGTTGTTGAGATATGGCTGTTACTTTTAAATGGACTGACTCCAAATCAGATGCATGTGA
TGATGTATGGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAATGATGCATTGGTTTTCT
TACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCGTGAATATGATCTTTGTA
TAGGACGTGTGTTGTCTATTATTTGTAGTAGTAACACATATCCAATACAGCTGTATGTTCTT
TTTCTTTTCTAATTTGGTGGCACTGGTATAACCAACACATTAAGTCAGTAGTACATTTTAA
TGAGGGTGGTTTTTTCTTTAAACACATGAACATTGTAAATGTGTTGGAAGAAAGTGTTTTA
AGAATAATAATTTGCAAATAAACTATTAATAAATATTATATGTGATAAATCTAAATATGA
ACATTAGAAATCTGTGGGCACATATTTTGGCTGATTGGTTAAAAATTTTAAACAGGTCCTTA
GCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATTTGTGATTAAAGTAAACTTTTAG
CTGTGTGTTCCCTTACTTCTAATACTGATTATGTTCTAAGCCTCCCCAAGTCCCAATGGAT
TTGCCTTCTCAAAATGTACAACCTAAGCACTAAAGAAAAATTAAGTGAAGTTGAAAAAT

374/550

FIGURE 374

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILV
KPKDVSLSWAAVKETWTWKHCDKAEFFSSSENVKVFESINMDTNDMWLMRKAYKYAFDKYRDQYNWFFLARPTTFAI
TENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSLNIPEKCPQGGMIWKISEDQLAV
CLKYAGVFAENAEDADGKDVNTKSVGLSIKEAMTYHPNQVVEGCCDMAVTENGLTPNQMHVMMYGVYRLRAFG
HIFNDALVFLPPNGSDND

Important features:**Signal sequence:**

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403,
409-413, 473-477, 729-733, 748-752**Tyrosine kinase phosphorylation site.**

amino acids 736-743

N-myristoylation site.amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564,
651-657, 657-663, 672-672**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

375/550

FIGURE 375

GTGTGTCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAAT
CTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAGAAGAAA
AAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGG
GCTGGGTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAA
AGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCCCTCAGGTGCACTATTGACAA
CCGGGTACCCGGGTGGCTTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTG
GTGCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCA
GAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCAACCCAAA
GACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAGATTCTTCAGATAT
CTCCATTAAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC
GGTTACTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA
AATTACAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGC
CGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATACTTTCAGAAGCCAA
GGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCT
AGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGT
GGAAAACAGACCTTTCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA
CTACACTTGCCTGGCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCC
AGCGCCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGCTCTGGCTGCTGCC
TCTTCTGGTCTTGACACCTGCTTCTCAAAATTTTGATGTGAGTGCCACTTCCCACCCGGGAAAG
GCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA
TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAA
GAATACTTTGGGGGAAAAAGAGTTTTAAAAAAGAAATTGAAATTTGCCTTGAGATATTTAGG
TACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCA
AGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCACAGA
GTGCCCCCAGTGGAACATTTCTGGAGCTGGCCATCCCAAATTCATCAGTCCATAGAGACGAA
CAGAATGAGACCTTCCGCCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACG
GCGTGTGTTGTGAACGTGAAATAAAAAGAGCAAAAAAAA

376/550

FIGURE 376

MKTIQPKMHNSISWAIETGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRV
TRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCSVQTDNHPKTS
RVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRRHISPKAVGFVSEDEYLEIQ
GITREQSGDYECASNDVAAPVVRVKVTVNYPPYISEAKGTGVFVGQKGTLCQCEASAVPSAE
FQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHNTNASIMLFGPGA
VSEVSNGTSRRAGCVWLLPLLVLHLLKF

Important features:**Signal peptide:**

amino acids 1-28

377/550

FIGURE 377

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTGCCCCCTTAGATTGTGAA
ATGTGGCTCAAGGCTTTCACAACCTTTCCCTTTCCTTTGCAACAGGTGCTTGCTCGGGGCTGAAG
GTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTCAC
TATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCACACA
ATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTCTGACTTGGAAATACCAACAC
AAGTTCACCATGATGCCACCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCCTGATGAA
GGCAATTACATCGTGAAGGTCAACATTGAGGGAATGGAACCTATCTGCCAGTCAGAAGATA
CAAGTCACGTTGATGATCCTGTCACAAAGCCAGTGGTGCAGATTATCTCCCTCTGGGGCT
GTGGAGTATGTGGGGAACATGACCCGTGACATGCCATGTGGAAGGGGGCACTCGGCTAGCTTAC
CAATGGCTAAAAAATGGGAGACCTGTCCACACAGCTCCACCTACTCCTTTTCTCCCCAAAC
AATACCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCTGCCTGGTGAGG
AACCTGTGAGTAAATGGAAAGTGATATCATTATGCCCATCATATATTATGGACCTTATGGA
CTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTCTTACTGTTGACCTTGGAGAG
GCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACTCCTGGATTAGGAGG
ACTGACAATACTACATATATCATTAGCATGGGCTCGCTTAGAAGTTGCATCTGAGAAAGTA
GCCCAGAAGACAATGGACTATGTGTCTGTGCTTACAACAACATAACCCGGCAGGCAAGATGAA
ACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTGACAGAAAGGAAAAATCA
TTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTGATTATATCCATGTGCTTCTC
TTCTTATGGAAAAAATATCAACCTTACAAAGTTATAAAACAGAACTAGAAAGGCAGGCCAGAA
ACAGAATACAGGAAAGCTCAAAACATTTTCAGGCCATGAAGATGCTCTGGATGACTTCGGAATA
TATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTCAGGATTCCAAGCAGGTCTGTTCCA
GCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGTGTATGAAGTTATTCAGCACATC
CCTGCCCAGCAGCAAGACCATCCAGAG**TGA**ACTTTTCATGGGCTAAACAGTACATTCGAGTGAA
ATCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGTATATTAATCTGGAATCAGTGAAGA
AACCAGGACCAACACCTTTACTCATTTATTCCTTTACATGCAGAATAGAGGCATTTATGCAAA
TTGAAGTGCAGGTTTTTCAGCATATACACAATGTCTTGTGCAACAGAAAAACATGTGGGGAA
ATATCTCCTCAGTGGAGAGTCGTTCTCATGCTGACGGGGAGAACGAAAGTGACAGGGGTTCTCT
CATAAGTTTTGTATGAATATCTCTACAACCTCAATTAGTTCTACTCTACACTTTCACTATC
ATCAACACTGAGACTATCCTGTCTCACCTACAAATGTGGAACTTTACATTTGTTGATTTTTT
AGCAGACTTTGTTTTATTAAATTTTTATTAGTGTTAAGAATGCTAAATTTATGTTTCAATTTT
ATTTCCAAATTTCTATCTTGTATTGTTGTACAACAAAGTAATAAGGATGGTTGTACAAAAACA
AACTATGCCTTCTCTTTTTTTCAATCACCAGTAGATTTTTTGAGAAGACTTGTGAACACTT
AAGGAATGACTATTAAAGTCTTATTTTTTTTCAAGGAAAGATGGATTCAAATAAATT
ATTCTGTTTTTGCTTTTAAAAA